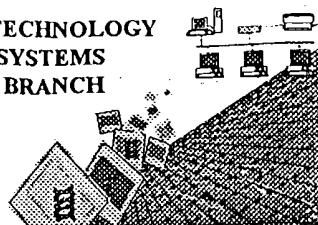# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/840,2770*

Source: *17 W/6*

Date Processed by STIC: *9/15/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/840,2770_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_/S__contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/840,277D**

DATE: 09/15/2004
TIME: 09:25:05

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\09152004\I840277D.raw**

```
 3 <110> APPLICANT: FEIGE, ULRICH
 4         KOHNO, TADAHIKO
 5         LACEY, DAVID
 6         BOONE, THOMAS CHARLES
 8 <120> TITLE OF INVENTION: ADHESION ANTAGONISTS (as amended)
10 <130> FILE REFERENCE: A-688A
12 <140> CURRENT APPLICATION NUMBER: US 09/840,277D
13 <141> CURRENT FILING DATE: 2001-04-23
15 <150> PRIOR APPLICATION NUMBER: US 60/198,919
16 <151> PRIOR FILING DATE: 2000-04-21
18 <150> PRIOR APPLICATION NUMBER: US 60/201,394
19 <151> PRIOR FILING DATE: 2000-05-03
21 <160> NUMBER OF SEQ ID NOS: 137
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 684
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(684)
35 <400> SEQUENCE: 1
36 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg        48
37 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
38 1               5                   10                  15
40 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc        96
41 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
42             20                  25                  30
44 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc       144
45 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
46         35                  40                  45
48 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag       192
49 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
50     50                  55                  60
52 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg       240
53 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
54 65                  70                  75                  80
56 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat       288
57 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
58             85                  90                  95
60 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc       336
61 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
62             100                 105                 110
```

RAW SEQUENCE LISTING   DATE: 09/15/2004
PATENT APPLICATION: US/09/840,277D   TIME: 09:25:05

Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\09152004\I840277D.raw

```
64 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag          384
65 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
66         115                 120                 125
68 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc          432
69 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
70     130                 135                 140
72 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg          480
73 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
74 145                 150                 155                 160
76 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct          528
77 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
78                 165                 170                 175
80 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc          576
81 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
82             180                 185                 190
84 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg          624
85 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
86         195                 200                 205
88 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg          672
89 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
90     210                 215                 220
92 tct ccg ggt aaa                                                          684
93 Ser Pro Gly Lys
94 225
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 228
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
104 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
105 1             5                 10                  15
108 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
109             20                 25                  30
112 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
113         35                 40                  45
116 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
117     50                 55                  60
120 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
121 65                 70                 75                  80
124 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
125             85                 90                  95
128 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
129             100                105                 110
132 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
133         115                120                 125
136 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
137     130                135                 140
140 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
141 145                150                155                 160
```

```
144 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
145             165                 170                 175
148 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
149             180                 185                 190
152 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
153         195                 200                 205
156 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
157     210                 215                 220
160 Ser Pro Gly Lys
161 225
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 8
166 <212> TYPE: PRT
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Preferred linker
172 <400> SEQUENCE: 3
174 Gly Gly Gly Lys Gly Gly Gly Gly
175 1               5
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 8
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Preferred linker
186 <400> SEQUENCE: 4
188 Gly Gly Gly Asn Gly Ser Gly Gly
189 1               5
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 8
194 <212> TYPE: PRT
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Preferred linker
200 <400> SEQUENCE: 5
202 Gly Gly Gly Cys Gly Gly Gly Gly
203 1               5
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 5
208 <212> TYPE: PRT
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Preferred linker
214 <400> SEQUENCE: 6
216 Gly Pro Asn Gly Gly
217 1               5
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 5
222 <212> TYPE: PRT
```

RAW SEQUENCE LISTING   DATE: 09/15/2004
PATENT APPLICATION: **US/09/840,277D**   TIME: 09:25:05

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\09152004\I840277D.raw**

```
223  <213> ORGANISM: Artificial Sequence
225  <220> FEATURE:
226  <223> OTHER INFORMATION: Laminin peptide
228  <400> SEQUENCE: 7
230  Tyr Ile Gly Ser Arg
231  1                   5
234  <210> SEQ ID NO: 8
235  <211> LENGTH: 49
236  <212> TYPE: PRT
237  <213> ORGANISM: Artificial Sequence
239  <220> FEATURE:
240  <223> OTHER INFORMATION: Echistatin peptide
242  <400> SEQUENCE: 8
244  Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
245  1               5                   10                  15
248  Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
249              20                  25                  30
252  Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
253              35                  40                  45
256  Thr
260  <210> SEQ ID NO: 9
261  <211> LENGTH: 7
262  <212> TYPE: PRT
263  <213> ORGANISM: Artificial Sequence
265  <220> FEATURE:
266  <223> OTHER INFORMATION: RGD, NGR derivative peptide
269  <220> FEATURE:
270  <221> NAME/KEY: misc_feature
271  <222> LOCATION: (2, 5 and)..(7)
272  <223> OTHER INFORMATION: Xaa is any amino acid
274  <400> SEQUENCE: 9
```
W--> **276 Arg Xaa Glu Thr Xaa Trp Xaa**
```
277  1               5
280  <210> SEQ ID NO: 10
282  <400> SEQUENCE: 10
```
W--> **283 000**
```
285  <210> SEQ ID NO: 11
286  <211> LENGTH: 9
287  <212> TYPE: PRT
288  <213> ORGANISM: Artificial Sequence
290  <220> FEATURE:
291  <223> OTHER INFORMATION: RGD, NGR derivative peptide
294  <220> FEATURE:
295  <221> NAME/KEY: misc_feature
296  <222> LOCATION: (2, 3, 7 and)..(8)
297  <223> OTHER INFORMATION: Xaa is any amino acid
299  <400> SEQUENCE: 11
```
W--> **301 Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys**
```
302  1               5
```

```
           RAW SEQUENCE LISTING              DATE: 09/15/2004
           PATENT APPLICATION:  US/09/840,277D    TIME: 09:25:05

           Input Set : A:\A-688A.ST25.txt
           Output Set: N:\CRF4\09152004\I840277D.raw
```

```
      305 <210> SEQ ID NO: 12
      307 <400> SEQUENCE: 12
W--> 308 000
      310 <210> SEQ ID NO: 13
      311 <211> LENGTH: 9
      312 <212> TYPE: PRT
      313 <213> ORGANISM: Artificial Sequence
      315 <220> FEATURE:
      316 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      319 <220> FEATURE:
      320 <221> NAME/KEY: misc_feature
      321 <222> LOCATION: (1, 2, 3, 7, 8 and)..(9)
      322 <223> OTHER INFORMATION: Xaa is any amino acid with Xaa at 1, 3, 7 and 9 capable of
      323       forming a bridge.
      325 <400> SEQUENCE: 13
W--> 327 Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa
      328 1               5
      331 <210> SEQ ID NO: 14
      332 <211> LENGTH: 17
      333 <212> TYPE: PRT
      334 <213> ORGANISM: Artificial Sequence
      336 <220> FEATURE:
      337 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      340 <220> FEATURE:
      341 <221> NAME/KEY: misc_feature
      342 <222> LOCATION: (2, 3, 4, 5, 6, 12, 13, 14, 15 and)..(16)
      343 <223> OTHER INFORMATION: At positions 2, 3, 4, 5, 6, 12, 13, 14, 15 and 16, Xaa is
any
      344       amino acid or may be absent.
      346 <400> SEQUENCE: 14
W--> 348 Cys Xaa Xaa Xaa Xaa Xaa Cys Arg Gly Asp Cys Xaa Xaa Xaa Xaa Xaa
      349 1               5                   10                  15
      352 Cys
      356 <210> SEQ ID NO: 15
      357 <211> LENGTH: 8
      358 <212> TYPE: PRT
      359 <213> ORGANISM: Artificial Sequence
      361 <220> FEATURE:
      362 <223> OTHER INFORMATION: RGD, NGR derivative peptide
      365 <220> FEATURE:
      366 <221> NAME/KEY: misc_feature
      367 <222> LOCATION: (1 and)..(8)
      368 <223> OTHER INFORMATION: Xaa is an independently selected amino acid.
      370 <220> FEATURE:
      371 <221> NAME/KEY: misc_feature
      372 <222> LOCATION: (2 and)..(7)
      373 <223> OTHER INFORMATION: Xaa equals 0 to 4 amino acids, each which is independently
      374       selected.
      376 <220> FEATURE:
      377 <221> NAME/KEY: misc_feature
```

file://C:\CRF4\OUTHOLD\Ver1840277D.htm   9/15/04

```
<210>  15
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  RGD, NGR derivative peptide


<220>
<221>  misc_feature
<222>  (1 and)..(8)
<223>  Xaa is an independently selected amino acid.

<220>
<221>  misc_feature
<222>  (2 and)..(7)
<223>  Xaa equals 0 to 4 amino acids, each which is independently
       selected.

<220>
<221>  misc_feature
<222>  (4)..(4)
<223>  Xaa is selected from the group consisting of glycine and leucine.

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa is selected from the group consisting of tryptophan and
       leucine.

<400>  15

Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa
1                   5
```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Same error in Sequence 16.

variable length is not permitted.

Xaa can only represent a single amino acid. (see item 5 on Error Summary Sheet)

Asp is at location 4

what about Xaa at location 6?

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\09152004\I840277D.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 2,5,7
Seq#:11; Xaa Pos. 2,3,7,8
Seq#:13; Xaa Pos. 1,2,3,7,8,9
Seq#:14; Xaa Pos. 2,3,4,5,6,12,13,14,15,16
Seq#:15; Xaa Pos. 1,2,5,6,7,8
Seq#:16; Xaa Pos. 1,2,3,6,7,8,9,10
Seq#:17; Xaa Pos. 3,5,6,13,15
Seq#:18; Xaa Pos. 2,3,4,7,15
Seq#:19; Xaa Pos. 3,4,5,6,8,13,15,18
Seq#:20; Xaa Pos. 2,5,6,7,12,13,14
Seq#:21; Xaa Pos. 1,3,6,9,12,13
Seq#:40; Xaa Pos. 3,4
Seq#:50; Xaa Pos. 2,3
Seq#:58; Xaa Pos. 5
Seq#:59; Xaa Pos. 6
Seq#:86; Xaa Pos. 3,15
Seq#:87; Xaa Pos. 13,15

VERIFICATION SUMMARY   DATE: 09/15/2004
PATENT APPLICATION: **US/09/840,277D**   TIME: 09:25:06

Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\09152004\I840277D.raw**

```
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:283 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:308 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
M:341 Repeated in SeqNo=19
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
```